



SEQUENCE LISTING

<110> FUJIWARA, TSUTOMU
WATANABE, TAKESHI
HORIE, MASATO

<120> HUMAN SKELETAL MUSCLE-SPECIFIC
UMBIQUITIN-CONJUGATING ENZYME

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<141> 2004-02-20

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<151> 2003-01-15

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<150> 09/055,699

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<150> 08/820,170

<151> 1997-03-19

<150> JP 63410/1996

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<150> JP 69163/1997

<151> 1997-03-05

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<170> PatentIn Ver. 2.1

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Asn Arg Asp Ser Ala Val Ala Ser Glu Tyr Glu Leu Val Gln Leu Leu	35	40	45		
Pro Gly Glu Arg Glu Leu Thr Ile Pro Ala Ser Ala Asn Val Phe Tyr	50	55	60		
Pro Met Asp Gly Ala Ser His Asp Phe Leu Leu Arg Gln Arg Arg Arg	65	70	75	80	
Ser Ser Thr Ala Thr Pro Gly Val Thr Ser Gly Pro Ser Ala Ser Gly	85	90	95		
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ctc ctg cgg cag cgg cga agg tcc tct act gct aca cct ggc gtc acc 294
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Ser Gly Pro Ser Ala Ser Gly Thr Pro Pro Ser Glu Gly Gly Gly Gly
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Gln Arg Gln Asp Thr Val Arg Ser Phe Leu Lys Arg Ser Lys Leu Gly
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Arg Tyr Asn Glu Glu Glu Arg Ala Gln Gln Glu Ala Glu Ala Ala Gln
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Pro Glu Glu Asp Tyr Gly Leu Asp Glu Ile	
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 Lys Pro Tyr Glu Cys Leu Asp Cys Gly Lys Ser Phe Ser Lys Lys Pro
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 Met Pro Ala Asp

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His Thr Gly Glu Lys Pro Tyr Gln Cys His Asn Cys Gly Lys Ser Phe							
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Phe Ala Ile Arg Ala Asp His Asp Phe Val Val Gln Glu Asp Phe Met
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Asp Tyr Lys Pro Val
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Leu Arg Glu Gln Leu Lys Glu Leu Thr Lys Gln Tyr Glu Lys Ser Glu
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Ser	Gln	Leu	Asp	Cys	Asn	Phe	Leu	Lys	Val	Val	Ser	Ser	Ser	Ile	Val	
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gac	aag	tac	att	ggt	gaa	agt	gct	cgt	ttg	atc	aga	gaa	atg	ttt	aat	676
Asp	Lys	Tyr	Ile	Gly	Glu	Ser	Ala	Arg	Leu	Ile	Arg	Glu	Met	Phe	Asn	
205					210					215					220	
tat	gct	aga	gat	cat	caa	cca	tgc	atc	att	ttt	atg	gat	gaa	ata	gat	724
Tyr	Ala	Arg	Asp	His	Gln	Pro	Cys	Ile	Ile	Phe	Met	Asp	Glu	Ile	Asp	
				225					230					235		
gct	att	ggt	ggt	cgt	cgg	ttt	tct	gag	ggt	act	tca	gct	gac	aga	gag	772

Ala	Ile	Gly	Gly	Arg	Arg	Phe	Ser	Glu	Gly	Thr	Ser	Ala	Asp	Arg	Glu	
			240					245					250			
att	cag	aga	acg	tta	atg	gag	tta	ctg	aat	caa	atg	gat	gga	ttt	gat	820
Ile	Gln	Arg	Thr	Leu	Met	Glu	Leu	Leu	Asn	Gln	Met	Asp	Gly	Phe	Asp	
		255					260					265				
act	ctg	cat	aga	gtt	aaa	atg	acc	atg	gct	aca	aac	aga	cca	gat	aca	868
Thr	Leu	His	Arg	Val	Lys	Met	Thr	Met	Ala	Thr	Asn	Arg	Pro	Asp	Thr	
		270				275					280					
ctg	gat	cct	gct	ttg	ctg	cgt	cca	gga	aga	tta	gat	aga	aaa	ata	cat	916
Leu	Asp	Pro	Ala	Leu	Leu	Arg	Pro	Gly	Arg	Leu	Asp	Arg	Lys	Ile	His	
285					290					295				300		
att	gat	ttg	cca	aat	gaa	caa	gca	aga	tta	gac	ata	ctg	aaa	atc	cat	964
Ile	Asp	Leu	Pro	Asn	Glu	Gln	Ala	Arg	Leu	Asp	Ile	Leu	Lys	Ile	His	
				305					310					315		
gca	ggt	ccc	att	aca	aag	cat	ggt	gaa	ata	gat	tat	gaa	gca	att	gtg	1012
Ala	Gly	Pro	Ile	Thr	Lys	His	Gly	Glu	Ile	Asp	Tyr	Glu	Ala	Ile	Val	
			320					325					330			
aag	ctt	tcg	gat	ggc	ttt	aat	gga	gca	gat	ctg	aga	aat	gtt	tgt	act	1060
Lys	Leu	Ser	Asp	Gly	Phe	Asn	Gly	Ala	Asp	Leu	Arg	Asn	Val	Cys	Thr	
		335					340					345				
gaa	gca	ggt	atg	ttc	gca	att	cgt	gct	gat	cat	gat	ttt	gta	gta	cag	1108
Glu	Ala	Gly	Met	Phe	Ala	Ile	Arg	Ala	Asp	His	Asp	Phe	Val	Val	Gln	
		350				355					360					
gaa	gac	ttc	atg	aaa	gca	gtc	aga	aaa	gtg	gct	gat	tct	aag	aag	ctg	1156
Glu	Asp	Phe	Met	Lys	Ala	Val	Arg	Lys	Val	Ala	Asp	Ser	Lys	Lys	Leu	
365					370				375						380	
gag	tct	aaa	ttg	gac	tac	aaa	cct	gtg	taatttactg	taagattttt						1203
Glu	Ser	Lys	Leu	Asp	Tyr	Lys	Pro	Val								
				385												
gatggctgca	tgacagatgt	tggttattg	taaaaataaa	gttaaagaaa	ataatgtatg											1263
tattggcaat	gatgtcatta	aaagtatatg	aataaaaaata	tgagtaacat	cataaaaatt											1323
agtaattcaa	cttttaagat	acagaagaaa	tttgatatgtt	tgttaaagtt	gcatttattg											1383
cagcaagtta	caaagggaaa	gtgttgaagc	ttttcatatt	tgctgcgtga	gcattttgta											1443

aaatattgaa agtgggtttga gatagtggta taagaaagca tttcttatga cttattttgt 1503
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 aaa 1566

<210> 16
 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 16
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 Ile Glu Ala Gln Ile Lys Ala Asn Tyr Asp Val Leu Glu Ser Gln Lys
 35 40 45
 Gly Ile Gly Met Asn Glu Pro Leu Val Asp Cys Glu Gly Tyr Pro Arg
 50 55 60
 Ser Asp Val Asp Leu Tyr Gln Val Arg Thr Ala Arg His Asn Ile Ile
 65 70 75 80
 Cys Leu Gln Asn Asp His Lys Ala Val Met Lys Gln Val Glu Glu Ala
 85 90 95
 Leu His Gln Leu His Ala Arg Asp Lys Glu Lys Gln Ala Arg Asp Met
 100 105 110
 Ala Glu Ala His Lys Glu Ala Met Ser Arg Lys Leu Gly Gln Ser Glu
 115 120 125
 Ser Gln Gly Pro Pro Arg Ala Phe Ala Lys Val Asn Ser Ile Ser Pro
 130 135 140
 Gly Ser Pro Ala Ser Ile Ala Gly Leu Gln Val Asp Asp Glu Ile Val
 145 150 155 160
 Glu Phe Gly Ser Val Asn Thr Gln Asn Phe Gln Ser Leu His Asn Ile
 165 170 175

Gly	Ser	Val	Val	Gln	His	Ser	Glu	Gly	Lys	Pro	Leu	Asn	Val	Thr	Val
			180					185					190		
Ile	Arg	Arg	Gly	Glu	Lys	His	Gln	Leu	Arg	Leu	Val	Pro	Thr	Arg	Trp
	195						200					205			
Ala	Gly	Lys	Gly	Leu	Leu	Gly	Cys	Asn	Ile	Ile	Pro	Leu	Gln	Arg	
	210					215					220				

<210> 17
 <211> 669
 <212> DNA
 <213> Homo sapiens

<400> 17
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 tatgacgtgc tggaaagcca aaaaggcatt gggatgaacg agccgctggg ggactgtgag 180
 ggctaccccc ggtcagacgt ggacctgtac caagtccgca ccgccaggca caacatcata 240
 tgcctgcaga atgatcaciaa ggcagtgatg aagcagggtg aggaggccct gcaccagctg 300
 cacgctcgcg acaaggagaa gcaggcccgg gacatggctg aggcccaciaa agaggccatg 360
 agccgcaaac tgggtcagag tgagagccag ggccctccac gggccttcgc caaagtgaac 420
 agcatcagcc ccggctcccc agccagcatc gcgggtctgc aagtggatga tgagattgtg 480
 gagttcggct ctgtgaacac ccagaacttc cagtcactgc ataacattgg cagtgtggtg 540
 cagcacagtg aggggaagcc cctgaatgtg acagtgatcc gcagggggga aaaacaccag 600
 cttagacttg ttccaacacg ctgggcagga aaaggactgc tgggctgcaa cattattcct 660
 ctgcaaaga 669

<210> 18
 <211> 1128
 <212> DNA
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<220>

<221> CDS

<222> (125)..(793)

<400> 18

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cacg atg tcc gac gag gaa gcg agg cag agc gga ggc tcc tcg cag gcc 169

Met Ser Asp Glu Glu Ala Arg Gln Ser Gly Gly Ser Ser Gln Ala

1

5

10

15

ggc gtc gtg act gtc agc gac gtc cag gag ctg atg cgg cgc aag gag 217

Gly Val Val Thr Val Ser Asp Val Gln Glu Leu Met Arg Arg Lys Glu

20

25

30

gag ata gaa gcg cag atc aag gcc aac tat gac gtg ctg gaa agc caa 265

Glu Ile Glu Ala Gln Ile Lys Ala Asn Tyr Asp Val Leu Glu Ser Gln

35

40

45

aaa ggc att ggg atg aac gag ccg ctg gtg gac tgt gag ggc tac ccc 313

Lys Gly Ile Gly Met Asn Glu Pro Leu Val Asp Cys Glu Gly Tyr Pro

50

55

60

cgg tca gac gtg gac ctg tac caa gtc cgc acc gcc agg cac aac atc 361

Arg Ser Asp Val Asp Leu Tyr Gln Val Arg Thr Ala Arg His Asn Ile

65

70

75

ata tgc ctg cag aat gat cac aag gca gtg atg aag cag gtg gag gag 409

Ile Cys Leu Gln Asn Asp His Lys Ala Val Met Lys Gln Val Glu Glu

80

85

90

95

gcc ctg cac cag ctg cac gct cgc gac aag gag aag cag gcc cgg gac 457

Ala Leu His Gln Leu His Ala Arg Asp Lys Glu Lys Gln Ala Arg Asp

100

105

110

atg gct gag gcc cac aaa gag gcc atg agc cgc aaa ctg ggt cag agt 505

Met Ala Glu Ala His Lys Glu Ala Met Ser Arg Lys Leu Gly Gln Ser

115

120

125

gag agc cag ggc cct cca cgg gcc ttc gcc aaa gtg aac agc atc agc 553

Glu Ser Gln Gly Pro Pro Arg Ala Phe Ala Lys Val Asn Ser Ile Ser

130

135

140

ccc ggc tcc cca gcc agc atc gcg ggt ctg caa gtg gat gat gag att	601
Pro Gly Ser Pro Ala Ser Ile Ala Gly Leu Gln Val Asp Asp Glu Ile	
145 150 155	
gtg gag ttc ggc tct gtg aac acc cag aac ttc cag tca ctg cat aac	649
Val Glu Phe Gly Ser Val Asn Thr Gln Asn Phe Gln Ser Leu His Asn	
160 165 170 175	
att ggc agt gtg gtg cag cac agt gag ggg aag ccc ctg aat gtg aca	697
Ile Gly Ser Val Val Gln His Ser Glu Gly Lys Pro Leu Asn Val Thr	
180 185 190	
gtg atc cgc agg ggg gaa aaa cac cag ctt aga ctt gtt cca aca cgc	745
Val Ile Arg Arg Gly Glu Lys His Gln Leu Arg Leu Val Pro Thr Arg	
195 200 205	
tgg gca gga aaa gga ctg ctg ggc tgc aac att att cct ctg caa aga	793
Trp Ala Gly Lys Gly Leu Leu Gly Cys Asn Ile Ile Pro Leu Gln Arg	
210 215 220	
tgattgtccc tggggaacag taacaggaaa gcattcttccc ttgccctgga cttgggtcta	853
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tcttaaaaac ttaggcttgg cctctttcac aaattaggcc acggccctaa ataggaattc	1033
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<210> 19
 <211> 506
 <212> PRT
 <213> Homo sapiens

<400> 19
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35

40

45

Ser Ser Thr Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser
50 55 60

Ser Gly Ser Thr Ser Ser Arg Ser Arg Leu Tyr Arg Lys Lys Arg Val
65 70 75 80

Pro Glu Pro Ser Arg Arg Ala Arg Arg Ala Pro Leu Gly Thr Asn Phe
85 90 95

Val Asp Arg Leu Pro Gln Ala Val Arg Asn Arg Val Gln Ala Leu Arg
100 105 110

Asn Ile Gln Asp Glu Cys Asp Lys Val Asp Thr Leu Phe Leu Lys Ala
115 120 125

Ile His Asp Leu Glu Arg Lys Tyr Ala Glu Leu Asn Lys Pro Leu Tyr
130 135 140

Asp Arg Arg Phe Gln Ile Ile Asn Ala Glu Tyr Glu Pro Thr Glu Glu
145 150 155 160

Glu Cys Glu Trp Asn Ser Glu Asp Glu Glu Phe Ser Ser Asp Glu Glu
165 170 175

Val Gln Asp Asn Thr Pro Ser Glu Met Pro Pro Leu Glu Gly Glu Glu
180 185 190

Glu Glu Asn Pro Lys Glu Asn Pro Glu Val Lys Ala Glu Glu Lys Glu
195 200 205

Val Pro Lys Glu Ile Pro Glu Val Lys Asp Glu Glu Lys Glu Val Ala
210 215 220

Lys Glu Ile Pro Glu Val Lys Ala Glu Glu Lys Ala Asp Ser Lys Asp
225 230 235 240

Cys Met Glu Ala Thr Pro Glu Val Lys Glu Asp Pro Lys Glu Val Pro
245 250 255

Gln Val Lys Ala Asp Asp Lys Glu Gln Pro Lys Ala Thr Glu Ala Lys
260 265 270

Ala Arg Ala Ala Val Arg Glu Thr His Lys Arg Val Pro Glu Glu Arg
275 280 285

Leu	Arg	Asp	Ser	Val	Asp	Leu	Lys	Arg	Ala	Arg	Lys	Gly	Lys	Pro	Lys	290	295	300
Arg	Glu	Asp	Pro	Lys	Gly	Ile	Pro	Asp	Tyr	Trp	Leu	Ile	Val	Leu	Lys	305	310	315
Asn	Val	Asp	Lys	Leu	Gly	Pro	Met	Ile	Gln	Lys	Tyr	Asp	Glu	Pro	Ile	325	330	335
Leu	Lys	Phe	Leu	Ser	Asp	Val	Ser	Leu	Lys	Phe	Ser	Lys	Pro	Gly	Gln	340	345	350
Pro	Val	Ser	Tyr	Thr	Phe	Glu	Phe	His	Phe	Leu	Pro	Asn	Pro	Tyr	Phe	355	360	365
Arg	Asn	Glu	Val	Leu	Val	Lys	Thr	Tyr	Ile	Ile	Lys	Ala	Lys	Pro	Asp	370	375	380
His	Asn	Asp	Pro	Phe	Phe	Ser	Trp	Gly	Trp	Glu	Ile	Glu	Asp	Cys	Lys	385	390	395
Gly	Cys	Lys	Ile	Asp	Arg	Arg	Arg	Gly	Lys	Asp	Val	Thr	Val	Thr	Thr	405	410	415
Thr	Gln	Ser	Arg	Thr	Thr	Ala	Thr	Gly	Glu	Ile	Glu	Ile	Gln	Pro	Arg	420	425	430
Val	Val	Pro	Asn	Ala	Ser	Phe	Phe	Asn	Phe	Phe	Ser	Pro	Pro	Glu	Ile	435	440	445
Pro	Met	Ile	Gly	Lys	Leu	Glu	Pro	Arg	Glu	Asp	Ala	Ile	Leu	Asp	Glu	450	455	460
Asp	Phe	Glu	Ile	Gly	Gln	Ile	Leu	His	Asp	Asn	Val	Ile	Leu	Lys	Ser	465	470	475
Ile	Tyr	Tyr	Tyr	Thr	Gly	Glu	Val	Asn	Gly	Thr	Tyr	Tyr	Gln	Phe	Gly	485	490	495
Lys	His	Tyr	Gly	Asn	Lys	Lys	Tyr	Arg	Lys							500	505	

<210> 20

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 20

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agcactagtg acagcagcag cagcagcagc actagtggca gcagcagcgg cagcggcagc 180
agcagcagca gcagcggcag cactagcagc cgcagccgct tgtatagaaa gaagagggta 240
cctgagcctt ccagaagggc gcggcggggc ccgttgggaa caaatttcgt ggataggctg 300
cctcaggcag ttagaaatcg tgtgcaagcg cttagaaaca ttcaagatga atgtgacaag 360
gtagataccc tgttcttaaa agcaattcat gatcttgaaa gaaaatatgc tgaactcaac 420
aagcctctgt atgataggcg gtttcaaadc atcaatgcag aatacgagcc tacagaagaa 480
gaatgtgaat ggaattcaga ggatgaggag ttcagcagtg atgaggaggt gcaggataac 540
acccttagtg aaatgcctcc cttagagggt gaggaagaag aaaaccctaa agaaaaccca 600
gagggtgaaag ctgaagagaa ggaagttcct aaagaaattc ctgagggtgaa ggatgaagaa 660
aaggaagttg ctaaagaaat tcctgaggta aaggctgaag aaaaagcaga ttctaaagac 720
tgtatggagg caaccctga agtaaaagaa gacctaagag aagtccccca ggtaaaggca 780
gatgataaag aacagcctaa agcaacagag gctaaggcaa gggctgcagt aagagagact 840
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aatgttgaca agctcggggc tatgattcag aagtatgatg agccatttct gaagttcttg 1020

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cattttctac ccaaccata cttcagaaat gaggtgctgg tgaagacata tataataaag 1140
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ggctgcaaga tagaccggag aagaggaaaa gatgttactg tgacaactac ccagagtcgc 1260
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acaactgcta ctggagaaat tgaaatccag ccaagagtgg ttctaatagc atcattcttc 1320
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atcctggatg aggactttga aattgggcag attttacatg ataatgtcat cctgaaatca 1440
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aacaagaaat acagaaaa                                     1518
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ccagctccgc tctgcgcgcg tgctgccatc gccgctgcca cctccgcagc ccgggcctcc 180
gccgccgcca cccaagcatc cgtgagtcac tttctgccca tctctggtcg cgcggtctcc 240
ctggtagagt ttgtaggctt gcaag atg gca gaa gca gat ttt aaa atg gtc 292
                Met Ala Glu Ala Asp Phe Lys Met Val
                1                      5
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act agt gat tct ggg gaa gaa tct gac agc agt agc tct agc agc agc 388
Thr Ser Asp Ser Gly Glu Glu Ser Asp Ser Ser Ser Ser Ser Ser
30 35 40

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Ser	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Thr	Ser	Ser	Arg	Ser	Arg	
		60						65				70				
ttg	tat	aga	aag	aag	agg	gta	cct	gag	cct	tcc	aga	agg	gcg	cgg	cgg	532
Leu	Tyr	Arg	Lys	Lys	Arg	Val	Pro	Glu	Pro	Ser	Arg	Arg	Ala	Arg	Arg	
		75				80					85					
gcc	ccg	ttg	gga	aca	aat	ttc	gtg	gat	agg	ctg	cct	cag	gca	gtt	aga	580
Ala	Pro	Leu	Gly	Thr	Asn	Phe	Val	Asp	Arg	Leu	Pro	Gln	Ala	Val	Arg	
		90			95					100					105	
aat	cgt	gtg	caa	gcg	ctt	aga	aac	att	caa	gat	gaa	tgt	gac	aag	gta	628
Asn	Arg	Val	Gln	Ala	Leu	Arg	Asn	Ile	Gln	Asp	Glu	Cys	Asp	Lys	Val	
			110						115					120		
gat	acc	ctg	ttc	tta	aaa	gca	att	cat	gat	ctt	gaa	aga	aaa	tat	gct	676
Asp	Thr	Leu	Phe	Leu	Lys	Ala	Ile	His	Asp	Leu	Glu	Arg	Lys	Tyr	Ala	
			125					130					135			
gaa	ctc	aac	aag	cct	ctg	tat	gat	agg	cgg	ttt	caa	atc	atc	aat	gca	724
Glu	Leu	Asn	Lys	Pro	Leu	Tyr	Asp	Arg	Arg	Phe	Gln	Ile	Ile	Asn	Ala	
		140					145					150				
gaa	tac	gag	cct	aca	gaa	gaa	gaa	tgt	gaa	tgg	aat	tca	gag	gat	gag	772
Glu	Tyr	Glu	Pro	Thr	Glu	Glu	Glu	Cys	Glu	Trp	Asn	Ser	Glu	Asp	Glu	
		155				160					165					
gag	ttc	agc	agt	gat	gag	gag	gtg	cag	gat	aac	acc	cct	agt	gaa	atg	820
Glu	Phe	Ser	Ser	Asp	Glu	Glu	Val	Gln	Asp	Asn	Thr	Pro	Ser	Glu	Met	
					175					180					185	
cct	ccc	tta	gag	ggt	gag	gaa	gaa	gaa	aac	cct	aaa	gaa	aac	cca	gag	868
Pro	Pro	Leu	Glu	Gly	Glu	Glu	Glu	Glu	Asn	Pro	Lys	Glu	Asn	Pro	Glu	
				190					195					200		
gtg	aaa	gct	gaa	gag	aag	gaa	gtt	cct	aaa	gaa	att	cct	gag	gtg	aag	916
Val	Lys	Ala	Glu	Glu	Lys	Glu	Val	Pro	Lys	Glu	Ile	Pro	Glu	Val	Lys	
			205					210					215			
gat	gaa	gaa	aag	gaa	gtt	gct	aaa	gaa	att	cct	gag	gta	aag	gct	gaa	964
Asp	Glu	Glu	Lys	Glu	Val	Ala	Lys	Glu	Ile	Pro	Glu	Val	Lys	Ala	Glu	
		220					225					230				
gaa	aaa	gca	gat	tct	aaa	gac	tgt	atg	gag	gca	acc	cct	gaa	gta	aaa	1012
Glu	Lys	Ala	Asp	Ser	Lys	Asp	Cys	Met	Glu	Ala	Thr	Pro	Glu	Val	Lys	

235	240	245	
gaa gat cct aaa gaa gtc ccc cag gta aag gca gat gat aaa gaa cag Glu Asp Pro Lys Glu Val Pro Gln Val Lys Ala Asp Asp Lys Glu Gln 250 255 260 265			1060
cct aaa gca aca gag gct aag gca agg gct gca gta aga gag act cat Pro Lys Ala Thr Glu Ala Lys Ala Arg Ala Ala Val Arg Glu Thr His 270 275 280			1108
aaa aga gtt cct gag gaa agg ctt cgg gac agt gta gat ctt aaa aga Lys Arg Val Pro Glu Glu Arg Leu Arg Asp Ser Val Asp Leu Lys Arg 285 290 295			1156
gct agg aag gga aag cct aaa aga gaa gac cct aaa ggc att cct gac Ala Arg Lys Gly Lys Pro Lys Arg Glu Asp Pro Lys Gly Ile Pro Asp 300 305 310			1204
tat tgg ctg att gtt tta aag aat gtt gac aag ctc ggg cct atg att Tyr Trp Leu Ile Val Leu Lys Asn Val Asp Lys Leu Gly Pro Met Ile 315 320 325			1252
cag aag tat gat gag ccc att ctg aag ttc ttg tcg gat gtt agc ctg Gln Lys Tyr Asp Glu Pro Ile Leu Lys Phe Leu Ser Asp Val Ser Leu 330 335 340 345			1300
aag ttc tca aaa cct ggc cag cct gta agt tac acc ttt gaa ttt cat Lys Phe Ser Lys Pro Gly Gln Pro Val Ser Tyr Thr Phe Glu Phe His 350 355 360			1348
ttt cta ccc aac cca tac ttc aga aat gag gtg ctg gtg aag aca tat Phe Leu Pro Asn Pro Tyr Phe Arg Asn Glu Val Leu Val Lys Thr Tyr 365 370 375			1396
ata ata aag gca aaa cca gat cac aat gat ccc ttc ttt tct tgg gga Ile Ile Lys Ala Lys Pro Asp His Asn Asp Pro Phe Phe Ser Trp Gly 380 385 390			1444
tgg gaa att gaa gat tgc aaa ggc tgc aag ata gac cgg aga aga gga Trp Glu Ile Glu Asp Cys Lys Gly Cys Lys Ile Asp Arg Arg Arg Gly 395 400 405			1492
aaa gat gtt act gtg aca act acc cag agt cgc aca act gct act gga Lys Asp Val Thr Val Thr Thr Thr Gln Ser Arg Thr Thr Ala Thr Gly 410 415 420 425			1540

gaa att gaa atc cag cca aga gtg gtt cct aat gca tca ttc ttc aac	1588
Glu Ile Glu Ile Gln Pro Arg Val Val Pro Asn Ala Ser Phe Phe Asn	
430 435 440	
ttc ttt agt cct cct gag att cct atg att ggg aag ctg gaa cca cga	1636
Phe Phe Ser Pro Pro Glu Ile Pro Met Ile Gly Lys Leu Glu Pro Arg	
445 450 455	
gaa gat gct atc ctg gat gag gac ttt gaa att ggg cag att tta cat	1684
Glu Asp Ala Ile Leu Asp Glu Asp Phe Glu Ile Gly Gln Ile Leu His	
460 465 470	
gat aat gtc atc ctg aaa tca atc tat tac tat act gga gaa gtc aat	1732
Asp Asn Val Ile Leu Lys Ser Ile Tyr Tyr Tyr Thr Gly Glu Val Asn	
475 480 485	
ggg acc tac tat caa ttt ggc aaa cat tat gga aac aag aaa tac aga	1780
Gly Thr Tyr Tyr Gln Phe Gly Lys His Tyr Gly Asn Lys Lys Tyr Arg	
490 495 500 505	
aaa taagtcaatc tgaaagattt ttcaagaatc ttaaaatctc aagaagtgaa	1833
Lys	
gcagattcat acagccttga aaaaagtaaa accctgacct gtaacctgaa cactattatt	1893
ccttatagtc aagtttttgt ggtttcttgg tagtctatat tttaaaaata gtcctaaaaa	1953
gtgtctaagt gccagtttat tctatctagg ctgttgtagt ataatatctt tcaaaatatg	2013
taagctgttg tcaattatct aaagcatggt agtttggtgc tacacagtgt tgatttttgt	2073
gatgtccttt ggtcatgttt ctggttagact gtagctgtga aactgtcaga attgttaact	2133
gaaacaaata tttgcttgaa aaaaaagtt catgaagtac caatgcaagt gttttatttt	2193
ttttcttttt tccagcccat aagactaagg gtttaaactt gcttgacta gctgtgcctt	2253
cattagtttg ctatagaaat ccagtactta tagtaaataa aacagtgtat tttgaagttt	2313
gactgcttga aaaagattag catacatcta atgtgaaaag accacatttg attcaactga	2373
gaccttgtgt atgtgacata tagtggccta taaatttaac cataatgatg ttattgttta	2433
ccactgaggt gttaatataa catagtattt ttgaaaaagt ttcttcatct tatattgtgt	2493
aattgtaaac taaagatacc gtgttttctt tgtattgtgt tctaccttcc ctttcaactga	2553

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aatattaaag tgtgttatac tat 2636

<210> 22

<211> 170

<212> PRT

<213> Homo sapiens

<400> 22

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Leu	Asn	Lys	Asn	Pro	Val	Glu	Gly	Phe	Ser	Ala	Gly	Leu	Ile	Asp	Asp
			20					25					30		

Asn	Asp	Leu	Tyr	Arg	Trp	Glu	Val	Leu	Ile	Ile	Gly	Pro	Pro	Asp	Thr
		35					40					45			

Leu	Tyr	Glu	Gly	Gly	Val	Phe	Lys	Ala	His	Leu	Thr	Phe	Pro	Lys	Asp
	50					55					60				

Tyr	Pro	Leu	Arg	Pro	Pro	Lys	Met	Lys	Phe	Ile	Thr	Glu	Ile	Trp	His
65					70					75					80

Pro	Asn	Val	Asp	Lys	Asn	Gly	Asp	Val	Cys	Ile	Ser	Ile	Leu	His	Glu
				85					90					95	

Pro	Gly	Glu	Asp	Lys	Tyr	Gly	Tyr	Glu	Lys	Pro	Glu	Glu	Arg	Trp	Leu
			100					105					110		

Pro	Ile	His	Thr	Val	Glu	Thr	Ile	Met	Ile	Ser	Val	Ile	Ser	Met	Leu
		115					120					125			

Ala	Asp	Pro	Asn	Gly	Asp	Ser	Pro	Ala	Asn	Val	Asp	Ala	Ala	Lys	Glu
	130					135					140				

Trp	Arg	Glu	Asp	Arg	Asn	Gly	Glu	Phe	Lys	Arg	Lys	Val	Ala	Arg	Cys
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Val	Arg	Lys	Ser	Gln	Glu	Thr	Ala	Phe	Glu
				165					170

<210> 23

<211> 510
<212> DNA
<213> Homo sapiens

<400> 23
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cttattattg gccctccaga tacactttat gaagggtggtg tttttaaggc tcattcttact 180
ttcccaaaag attatcccct ccgacctcct aaaatgaaat tcattacaga aatctggcac 240
ccaaatggtg ataaaaatgg tgatgtgtgc atttctattc ttcatgagcc tggggaagat 300
aagtatgggtt atgaaaagcc agaggaacgc tggctcccta tccacactgt ggaaaccatc 360
atgattagtg tcatttctat gctggcagac cctaattggag actcacctgc taatgttgat 420
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gtaagaaaaa gccaaagagac tgcttttgag 510

<210> 24
<211> 617
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (19)..(528)

<400> 24
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1 5 10
aga cag ctg gca gaa ctc aac aaa aat cca gtg gaa ggc ttt tct gca 99
Arg Gln Leu Ala Glu Leu Asn Lys Asn Pro Val Glu Gly Phe Ser Ala
15 20 25
ggt tta ata gat gac aat gat ctc tac cga tgg gaa gtc ctt att att 147
Gly Leu Ile Asp Asp Asn Asp Leu Tyr Arg Trp Glu Val Leu Ile Ile
30 35 40

ggc cct cca gat aca ctt tat gaa ggt ggt gtt ttt aag gct cat ctt	195
Gly Pro Pro Asp Thr Leu Tyr Glu Gly Gly Val Phe Lys Ala His Leu	
45 50 55	
act ttc cca aaa gat tat ccc ctc cga cct cct aaa atg aaa ttc att	243
Thr Phe Pro Lys Asp Tyr Pro Leu Arg Pro Pro Lys Met Lys Phe Ile	
60 65 70 75	
aca gaa atc tgg cac cca aat gtt gat aaa aat ggt gat gtg tgc att	291
Thr Glu Ile Trp His Pro Asn Val Asp Lys Asn Gly Asp Val Cys Ile	
80 85 90	
tct att ctt cat gag cct ggg gaa gat aag tat ggt tat gaa aag cca	339
Ser Ile Leu His Glu Pro Gly Glu Asp Lys Tyr Gly Tyr Glu Lys Pro	
95 100 105	
gag gaa cgc tgg ctc cct atc cac act gtg gaa acc atc atg att agt	387
Glu Glu Arg Trp Leu Pro Ile His Thr Val Glu Thr Ile Met Ile Ser	
110 115 120	
gtc att tct atg ctg gca gac cct aat gga gac tca cct gct aat gtt	435
Val Ile Ser Met Leu Ala Asp Pro Asn Gly Asp Ser Pro Ala Asn Val	
125 130 135	
gat gct gcg aaa gaa tgg agg gaa gat aga aat gga gaa ttt aaa aga	483
Asp Ala Ala Lys Glu Trp Arg Glu Asp Arg Asn Gly Glu Phe Lys Arg	
140 145 150 155	
aaa gtt gcc cgc tgt gta aga aaa agc caa gag act gct ttt gag	528
Lys Val Ala Arg Cys Val Arg Lys Ser Gln Glu Thr Ala Phe Glu	
160 165 170	
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gcactgtttt tcctgcactc taccacccg	617

<210> 25
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 25
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 1 5 10 15

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			20					25					30		
Ala	Arg	Pro	Val	Lys	Leu	Ala	Ala	Phe	Pro	Thr	Ser	Leu	Ser	Asp	Cys
		35					40					45			
Gln	Thr	Pro	Thr	Gly	Trp	Asn	Cys	Ser	Gly	Tyr	Asp	Asp	Arg	Glu	Asn
	50					55					60				
Asp	Leu	Phe	Leu	Cys	Asp	Thr	Asn	Thr	Cys	Lys	Phe	Asp	Gly	Glu	Cys
65					70					75					80
Leu	Arg	Ile	Gly	Asp	Thr	Val	Thr	Cys	Val	Cys	Gln	Phe	Lys	Cys	Asn
				85					90					95	
Asn	Asp	Tyr	Val	Pro	Val	Cys	Gly	Ser	Asn	Gly	Glu	Ser	Tyr	Gln	Asn
			100					105					110		
Glu	Cys	Tyr	Leu	Arg	Gln	Ala	Ala	Cys	Lys	Gln	Gln	Ser	Glu	Ile	Leu
		115					120					125			
Val	Val	Ser	Glu	Gly	Ser	Cys	Ala	Thr	Asp	Ala	Gly	Ser	Gly	Ser	Gly
	130					135					140				
Asp	Gly	Val	His	Glu	Gly	Ser	Gly	Glu	Thr	Ser	Gln	Lys	Glu	Thr	Ser
145					150					155					160
Thr	Cys	Asp	Ile	Cys	Gln	Phe	Gly	Ala	Glu	Cys	Asp	Glu	Asp	Ala	Glu
				165					170					175	
Asp	Val	Trp	Cys	Val	Cys	Asn	Ile	Asp	Cys	Ser	Gln	Thr	Asn	Phe	Asn
			180					185					190		
Pro	Leu	Cys	Ala	Ser	Asp	Gly	Lys	Ser	Tyr	Asp	Asn	Ala	Cys	Gln	Ile
		195					200					205			
Lys	Glu	Ala	Ser	Cys	Gln	Lys	Gln	Glu	Lys	Ile	Glu	Val	Met	Ser	Leu
	210					215					220				
Gly	Arg	Cys	Gln	Asp	Asn	Thr	Thr	Thr	Thr	Thr	Lys	Ser	Glu	Asp	Gly
225					230					235					240
His	Tyr	Ala	Arg	Thr	Asp	Tyr	Ala	Glu	Asn	Ala	Asn	Lys	Leu	Glu	Glu
				245					250					255	

Ser Ala Arg Glu His His Ile Pro Cys Pro Glu His Tyr Asn Gly Phe
 260 265 270
 Cys Met His Gly Lys Cys Glu His Ser Ile Asn Met Gln Glu Pro Ser
 275 280 285
 Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His Cys Glu Lys Lys Asp
 290 295 300
 Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val Arg Phe Gln Tyr Val
 305 310 315 320
 Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile Ala Val Ile Cys Val
 325 330 335
 Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg Ser Asn Arg Ile His
 340 345 350
 Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser Asp Asn Thr Thr Arg
 355 360 365
 Ala Ser Thr Arg Leu Ile
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<210> 26

<211> 1122

<212> DNA

<213> Homo sapiens

<400> 26

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 ttccctacct ccttaagtga ctgccaaacg cccaccggct ggaattgctc tggttatgat 180
 gacagagaaa atgatctctt cctctgtgac accaacacct gtaaatttga tggggaatgt 240
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 cctgtgtgtg gctccaatgg ggagagctac cagaatgagt gttacctgcg acaggctgca 360
 tgcaaacagc agagtgagat acttgtggtg tcagaaggat catgtgccac agatgcagga 420
 tcaggatctg gagatggagt ccatgaaggc tctggagaaa ctagtcaaaa ggagacatcc 480

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acctgtgata tttgccagtt tgggtgcagaa tgtgacgaag atgccgagga tgtctgggtgt 540
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tcttatgata atgcatgcca aatcaaagaa gcatcgtgtc agaaacagga gaaaattgaa 660
gtcatgtctt tgggtcgatg tcaagataac acaactacaa ctactaagtc tgaagatggg 720
cattatgcaa gaacagatta tgcagagaat gctaacaat tagaagaaag tgccagagaa 780
caccacatac cttgtccgga acattacaat ggcttctgca tgcatgggaa gtgtgagcat 840

tctatcaata tgcaggagcc atcttgcagg tgtgatgctg gttatactgg acaacactgt 900
gaaaaaaagg actacagtgt tctatacgtt gtccccggtc ctgtacgatt tcagtatgtc 960
ttaatcgcag ctgtgattgg aacaattcag attgctgtca tctgtgtggt ggtcctctgc 1020
atcacaagga aatgccccag aagcaacaga attcacagac agaagcaaaa tacagggcac 1080
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<210> 27
<211> 1721
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (368) .. (1489)

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<400> 27
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cccgcgtctc cggcgcagct tctcagcggg cgaccctctc gctccggggc tgagccagtc 180
cctggatggtt gctgaaactc tcgagatcat gcgcggggtt ggctgctgct tccccgccgg 240
gtgccactgc caccgccgcc gcctctgctg ccgcgcgtccg cgggatgctc agtagcccg 300
tgccccggccc ccgcgatact gtgttcctcg gaagccggtt gctgctgcag agttgcacga 360

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actagtc	atg	gtg	ctg	tgg	gag	tcc	ccg	cgg	cag	tgc	agc	agc	tgg	aca	409	
	Met	Val	Leu	Trp	Glu	Ser	Pro	Arg	Gln	Cys	Ser	Ser	Trp	Thr		
	1				5					10						
ctt	tgc	gag	ggc	ttt	tgc	tgg	ctg	ctg	ctg	ctg	ccc	gtc	atg	cta	ctc	457
Leu	Cys	Glu	Gly	Phe	Cys	Trp	Leu	Leu	Leu	Leu	Pro	Val	Met	Leu	Leu	
15					20					25					30	
atc	gta	gcc	cgc	ccg	gtg	aag	ctc	gct	gct	ttc	cct	acc	tcc	tta	agt	505
Ile	Val	Ala	Arg	Pro	Val	Lys	Leu	Ala	Ala	Phe	Pro	Thr	Ser	Leu	Ser	
				35					40					45		
gac	tgc	caa	acg	ccc	acc	ggc	tgg	aat	tgc	tct	ggc	tat	gat	gac	aga	553
Asp	Cys	Gln	Thr	Pro	Thr	Gly	Trp	Asn	Cys	Ser	Gly	Tyr	Asp	Asp	Arg	
			50					55					60			
gaa	aat	gat	ctc	ttc	ctc	tgt	gac	acc	aac	acc	tgt	aaa	ttt	gat	ggg	601
Glu	Asn	Asp	Leu	Phe	Leu	Cys	Asp	Thr	Asn	Thr	Cys	Lys	Phe	Asp	Gly	
		65					70					75				
gaa	tgt	tta	aga	att	gga	gac	act	gtg	act	tgc	gtc	tgt	cag	ttc	aag	649
Glu	Cys	Leu	Arg	Ile	Gly	Asp	Thr	Val	Thr	Cys	Val	Cys	Gln	Phe	Lys	
	80					85					90					
tgc	aac	aat	gac	tat	gtg	cct	gtg	tgt	ggc	tcc	aat	ggg	gag	agc	tac	697
Cys	Asn	Asn	Asp	Tyr	Val	Pro	Val	Cys	Gly	Ser	Asn	Gly	Glu	Ser	Tyr	
95					100					105					110	
cag	aat	gag	tgt	tac	ctg	cga	cag	gct	gca	tgc	aaa	cag	cag	agt	gag	745
Gln	Asn	Glu	Cys	Tyr	Leu	Arg	Gln	Ala	Ala	Cys	Lys	Gln	Gln	Ser	Glu	
				115					120					125		
ata	ctt	gtg	gtg	tca	gaa	gga	tca	tgt	gcc	aca	gat	gca	gga	tca	gga	793
Ile	Leu	Val	Val	Ser	Glu	Gly	Ser	Cys	Ala	Thr	Asp	Ala	Gly	Ser	Gly	
			130					135					140			
tct	gga	gat	gga	gtc	cat	gaa	ggc	tct	gga	gaa	act	agt	caa	aag	gag	841
Ser	Gly	Asp	Gly	Val	His	Glu	Gly	Ser	Gly	Glu	Thr	Ser	Gln	Lys	Glu	
		145					150					155				
aca	tcc	acc	tgt	gat	att	tgc	cag	ttt	ggc	gca	gaa	tgt	gac	gaa	gat	889
Thr	Ser	Thr	Cys	Asp	Ile	Cys	Gln	Phe	Gly	Ala	Glu	Cys	Asp	Glu	Asp	
	160					165					170					
gcc	gag	gat	gtc	tgg	tgt	gtg	tgt	aat	att	gac	tgt	tct	caa	acc	aac	937

Ala 175	Glu	Asp	Val	Trp	Cys 180	Val	Cys	Asn	Ile	Asp 185	Cys	Ser	Gln	Thr	Asn 190	
ttc	aat	ccc	ctc	tgc	gct	tct	gat	ggg	aaa	tct	tat	gat	aat	gca	tgc	985
Phe	Asn	Pro	Leu	Cys 195	Ala	Ser	Asp	Gly	Lys 200	Ser	Tyr	Asp	Asn	Ala 205	Cys	
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Gln	Ile	Lys	Glu	Ala	Ser	Cys	Gln	Lys 215	Gln	Glu	Lys	Ile	Glu	Val 220	Met	
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Ser	Leu	Gly 225	Arg	Cys	Gln	Asp	Asn 230	Thr	Thr	Thr	Thr	Thr	Lys 235	Ser	Glu	
gat	ggg	cat	tat	gca	aga	aca	gat	tat	gca	gag	aat	gct	aac	aaa	tta	1129
Asp	Gly 240	His	Tyr	Ala	Arg	Thr	Asp 245	Tyr	Ala	Glu	Asn 250	Ala	Asn	Lys	Leu	
gaa	gaa	agt	gcc	aga	gaa	cac	cac	ata	cct	tgt	ccg	gaa	cat	tac	aat	1177
Glu 255	Glu	Ser	Ala	Arg	Glu	His	His 260	Ile	Pro	Cys 265	Pro	Glu	His	Tyr	Asn 270	
ggc	ttc	tgc	atg	cat	ggg	aag	tgt	gag	cat	tct	atc	aat	atg	cag	gag	1225
Gly	Phe	Cys	Met	His 275	Gly	Lys	Cys	Glu	His 280	Ser	Ile	Asn	Met	Gln 285	Glu	
cca	tct	tgc	agg	tgt	gat	gct	ggg	tat	act	gga	caa	cac	tgt	gaa	aaa	1273
Pro	Ser	Cys	Arg 290	Cys	Asp	Ala	Gly	Tyr 295	Thr	Gly	Gln	His	Cys 300	Glu	Lys	
aag	gac	tac	agt	gtt	cta	tac	gtt	gtt	ccc	ggg	cct	gta	cga	ttt	cag	1321
Lys	Asp	Tyr 305	Ser	Val	Leu	Tyr	Val 310	Val	Pro	Gly	Pro	Val 315	Arg	Phe	Gln	
tat	gtc	tta	atc	gca	gct	gtg	att	gga	aca	att	cag	att	gct	gtc	atc	1369
Tyr	Val 320	Leu	Ile	Ala	Ala	Val	Ile 325	Gly	Thr	Ile	Gln 330	Ile	Ala	Val	Ile	
tgt	gtg	gtg	gtc	ctc	tgc	atc	aca	agg	aaa	tgc	ccc	aga	agc	aac	aga	1417
Cys 335	Val	Val	Val	Leu	Cys 340	Ile	Thr	Arg	Lys	Cys 345	Pro	Arg	Ser	Asn	Arg 350	
att	cac	aga	cag	aag	caa	aat	aca	ggg	cac	tac	agt	tca	gac	aat	aca	1465
Ile	His	Arg	Gln	Lys 355	Gln	Asn	Thr	Gly	His 360	Tyr	Ser	Ser	Asp	Asn 365	Thr	

aca aga gcg tcc acg agg tta atc taaagggagc atgtttcaca gtggctggac 1519
 Thr Arg Ala Ser Thr Arg Leu Ile
 370

taccgagagc ttggactaca caatacagta ttatagacaa aagaataaga caagagatct 1579
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<210> 28
 <211> 817
 <212> PRT
 <213> Homo sapiens

<400> 28
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 Pro Thr Ser Gly Pro Pro Gly Asn Asn Gly Gly Ser Leu Leu Ser Val
 20 25 30
 Ile Thr Glu Gly Val Gly Glu Leu Ser Val Ile Asp Pro Glu Val Ala
 35 40 45
 Gln Lys Ala Cys Gln Glu Val Leu Glu Lys Val Lys Leu Leu His Gly
 50 55 60
 Gly Val Ala Val Ser Ser Arg Gly Thr Pro Leu Glu Leu Val Asn Gly
 65 70 75 80
 Asp Gly Val Asp Ser Glu Ile Arg Cys Leu Asp Asp Pro Pro Ala Gln
 85 90 95
 Ile Arg Glu Glu Glu Asp Glu Met Gly Ala Ala Val Ala Ser Gly Thr
 100 105 110
 Ala Lys Gly Ala Arg Arg Arg Arg Gln Asn Asn Ser Ala Lys Gln Ser
 115 120 125
 Trp Leu Leu Arg Leu Phe Glu Ser Lys Leu Phe Asp Ile Ser Met Ala
 130 135 140

Ile	Ser	Tyr	Leu	Tyr	Asn	Ser	Lys	Glu	Pro	Gly	Val	Gln	Ala	Tyr	Ile	145	150	155	160
Gly	Asn	Arg	Leu	Phe	Cys	Phe	Arg	Asn	Glu	Asp	Val	Asp	Phe	Tyr	Leu	165	170	175	
Pro	Gln	Leu	Leu	Asn	Met	Tyr	Ile	His	Met	Asp	Glu	Asp	Val	Gly	Asp	180	185	190	
Ala	Ile	Lys	Pro	Tyr	Ile	Val	His	Arg	Cys	Arg	Gln	Ser	Ile	Asn	Phe	195	200	205	
Ser	Leu	Gln	Cys	Ala	Leu	Leu	Leu	Gly	Ala	Tyr	Ser	Ser	Asp	Met	His	210	215	220	
Ile	Ser	Thr	Gln	Arg	His	Ser	Arg	Gly	Thr	Lys	Leu	Arg	Lys	Leu	Ile	225	230	235	240
Leu	Ser	Asp	Glu	Leu	Lys	Pro	Ala	His	Arg	Lys	Arg	Glu	Leu	Pro	Ser	245	250	255	
Leu	Ser	Pro	Ala	Pro	Asp	Thr	Gly	Leu	Ser	Pro	Ser	Lys	Arg	Thr	His	260	265	270	
Gln	Arg	Ser	Lys	Ser	Asp	Ala	Thr	Ala	Ser	Ile	Ser	Leu	Ser	Ser	Asn	275	280	285	
Leu	Lys	Arg	Thr	Ala	Ser	Asn	Pro	Lys	Val	Glu	Asn	Glu	Asp	Glu	Glu	290	295	300	
Leu	Ser	Ser	Ser	Thr	Glu	Ser	Ile	Asp	Asn	Ser	Phe	Ser	Ser	Pro	Val	305	310	315	320
Arg	Leu	Ala	Pro	Glu	Arg	Glu	Phe	Ile	Lys	Ser	Leu	Met	Ala	Ile	Gly	325	330	335	
Lys	Arg	Leu	Ala	Thr	Leu	Pro	Thr	Lys	Glu	Gln	Lys	Thr	Gln	Arg	Leu	340	345	350	
Ile	Ser	Glu	Leu	Ser	Leu	Leu	Asn	His	Lys	Leu	Pro	Ala	Arg	Val	Trp	355	360	365	
Leu	Pro	Thr	Ala	Gly	Phe	Asp	His	His	Val	Val	Arg	Val	Pro	His	Thr	370	375	380	

Gln	Ala	Val	Val	Leu	Asn	Ser	Lys	Asp	Lys	Ala	Pro	Tyr	Leu	Ile	Tyr	385	390	395	400
Val	Glu	Val	Leu	Glu	Cys	Glu	Asn	Phe	Asp	Thr	Thr	Ser	Val	Pro	Ala	405	410	415	
Arg	Ile	Pro	Glu	Asn	Arg	Ile	Arg	Ser	Thr	Arg	Ser	Val	Glu	Asn	Leu	420	425	430	
Pro	Glu	Cys	Gly	Ile	Thr	His	Glu	Gln	Arg	Ala	Gly	Ser	Phe	Ser	Thr	435	440	445	
Val	Pro	Asn	Tyr	Asp	Asn	Asp	Asp	Glu	Ala	Trp	Ser	Val	Asp	Asp	Ile	450	455	460	
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Asn	Ile	Ser	Gln	Phe	Ser	Val	Asp	Ser	Ile	Thr	Ser	Gln	Glu	Ser	Lys	485	490	495	
Glu	Pro	Val	Phe	Ile	Ala	Ala	Gly	Asp	Ile	Arg	Arg	Arg	Leu	Ser	Glu	500	505	510	
Gln	Leu	Ala	His	Thr	Pro	Thr	Ala	Phe	Lys	Arg	Asp	Pro	Glu	Asp	Pro	515	520	525	
Ser	Ala	Val	Ala	Leu	Lys	Glu	Pro	Trp	Gln	Glu	Lys	Val	Arg	Arg	Ile	530	535	540	
Arg	Glu	Gly	Ser	Pro	Tyr	Gly	His	Leu	Pro	Asn	Trp	Arg	Leu	Leu	Ser	545	550	555	560
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Lys	Gln	Ser	Gln	Leu	Ser	Leu	Leu	Asp	Tyr	Phe	Leu	Gln	Glu	His	Gly	625	630	635	640
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Gly	Leu	Asp	Gly	Asp	Met	Phe	Asn	Tyr	Tyr	Lys	Met	Leu	Met	Leu	Gln	725	730	735	
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Glu	Ile	Met	Gln	Gln	Gly	Ser	Gln	Leu	Pro	Cys	Phe	His	Gly	Ser	Ser	755	760	765	
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Gln	Leu	Gln	Leu	Leu	Val	Glu	Gln	Met	Val	Asp	Gly	Ser	Met	Arg	Ser	785	790	795	800
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<212> DNA

<213> Homo sapiens

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Ser Glu Pro Thr Ser Gly Pro Pro Gly Asn Asn Gly Gly Ser Leu Leu
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Val Ala Gln Lys Ala Cys Gln Glu Val Leu Glu Lys Val Lys Leu Leu
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His Gly Gly Val Ala Val Ser Ser Arg Gly Thr Pro Leu Glu Leu Val
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Asn Gly Asp Gly Val Asp Ser Glu Ile Arg Cys Leu Asp Asp Pro Pro
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<211> 816

<212> PRT

<213> Homo sapiens

<400> 37

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			20					25					30					
Leu	Thr	Glu	Leu	Glu	Leu	Gly	Glu	Ser	Thr	Thr	Gly	Val	Arg	Gln	Val			
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Pro	Gly	Leu	His	Asn	Gly	Thr	Lys	Ala	Phe	Leu	Phe	Gln	Asp	Thr	Pro			
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Arg	Ser	Ile	Lys	Ala	Ser	Thr	Ala	Thr	Ala	Glu	Gln	Phe	Phe	Gln	Lys			
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Leu	Arg	Asn	Lys	His	Glu	Phe	Thr	Ile	Leu	Val	Thr	Leu	Lys	Gln	Thr			
				85					90					95				
His	Leu	Asn	Ser	Gly	Val	Ile	Leu	Ser	Ile	His	His	Leu	Asp	His	Arg			
			100					105					110					
Tyr	Leu	Glu	Leu	Glu	Ser	Ser	Gly	His	Arg	Asn	Glu	Val	Arg	Leu	His			
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	130					135					140							
Leu	Ala	Asp	Asp	Lys	Trp	His	Lys	Leu	Ser	Leu	Ala	Ile	Ser	Ala	Ser			
145					150					155					160			
His	Leu	Ile	Leu	His	Ile	Asp	Cys	Asn	Lys	Ile	Tyr	Glu	Arg	Val	Val			
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			260					265					270				
Thr	Cys	Thr	Met	Lys	Gly	Thr	Thr	Tyr	Arg	Glu	Phe	Glu	Ser	Trp	Ile		
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Asp	Gly	Cys	Lys	Asn	Cys	Thr	Cys	Leu	Asn	Gly	Thr	Ile	Gln	Cys	Glu		
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Thr	Glu	His	Asp	Glu	Cys	Ile	Thr	Asn	Gln	His	Asn	Cys	Asp	Glu	Asn		
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<210> 38

<211> 2448

<212> DNA

<213> Homo sapiens

<400> 38

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Ile	Leu	Ser	Ile	His	His	Leu	Asp	His	Arg	Tyr	Leu	Glu	Leu	Glu	Ser	
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Ser	Gly	His	Arg	Asn	Glu	Val	Arg	Leu	His	Tyr	Arg	Ser	Gly	Ser	His	
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Arg	Pro	His	Thr	Glu	Val	Phe	Pro	Tyr	Ile	Leu	Ala	Asp	Asp	Lys	Trp	
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His	Lys	Leu	Ser	Leu	Ala	Ile	Ser	Ala	Ser	His	Leu	Ile	Leu	His	Ile	
				155					160					165		
gac	tgc	aat	aaa	att	tat	gaa	agg	gta	gta	gaa	aag	ccc	tcc	aca	gac	642
Asp	Cys	Asn	Lys	Ile	Tyr	Glu	Arg	Val	Val	Glu	Lys	Pro	Ser	Thr	Asp	
			170					175					180			
ttg	cct	cta	ggc	aca	aca	ttt	tgg	cta	gga	cag	aga	aat	aat	gcg	cat	690
Leu	Pro	Leu	Gly	Thr	Thr	Phe	Trp	Leu	Gly	Gln	Arg	Asn	Asn	Ala	His	
		185					190					195				
gga	tat	ttt	aag	ggt	ata	atg	caa	gat	gtc	caa	tta	ctt	gtc	atg	ccc	738
Gly	Tyr	Phe	Lys	Gly	Ile	Met	Gln	Asp	Val	Gln	Leu	Leu	Val	Met	Pro	
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cag	gga	ttt	att	gct	cag	tgc	cca	gat	ctt	aat	cgc	acc	tgt	cca	act	786
Gln	Gly	Phe	Ile	Ala	Gln	Cys	Pro	Asp	Leu	Asn	Arg	Thr	Cys	Pro	Thr	
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tgc	aat	gac	ttc	cat	gga	ctt	gtg	cag	aaa	atc	atg	gag	cta	cag	gat	834
Cys	Asn	Asp	Phe	His	Gly	Leu	Val	Gln	Lys	Ile	Met	Glu	Leu	Gln	Asp	
				235					240					245		
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Ile	Leu	Ala	Lys	Thr	Ser	Ala	Lys	Leu	Ser	Arg	Ala	Glu	Gln	Arg	Met	
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Thr	Thr	Tyr	Arg	Glu	Phe	Glu	Ser	Trp	Ile	Asp	Gly	Cys	Lys	Asn	Cys	
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Pro	Asp	Cys	Pro	Leu	Lys	Ser	Ala	Leu	Ala	Tyr	Val	Asp	Gly	Lys	Cys	
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Cys	Lys	Glu	Cys	Lys	Ser	Ile	Cys	Gln	Phe	Gln	Gly	Arg	Thr	Tyr	Phe	
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gaa	gga	gaa	aga	aat	aca	gtc	tat	tcc	tct	tct	gga	gta	tgt	gtt	ctc	1170
Glu	Gly	Glu	Arg	Asn	Thr	Val	Tyr	Ser	Ser	Ser	Gly	Val	Cys	Val	Leu	
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Tyr	Glu	Cys	Lys	Asp	Gln	Thr	Met	Lys	Leu	Val	Glu	Ser	Ser	Gly	Cys	
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cca	gct	ttg	gat	tgt	cca	gag	tct	cat	cag	ata	acc	ttg	tct	cac	agc	1266
Pro	Ala	Leu	Asp	Cys	Pro	Glu	Ser	His	Gln	Ile	Thr	Leu	Ser	His	Ser	
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Cys	Met	Glu	Asn	Ser	Ile	Cys	Arg	Asn	Leu	Asn	Asp	Arg	Ala	Val	Cys	
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Ser	Cys	Arg	Asp	Gly	Phe	Arg	Ala	Leu	Arg	Glu	Asp	Asn	Ala	Tyr	Cys	
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Ile Thr Asn Gln His Asn Cys Asp Glu Asn Ala Leu Cys Phe Asn Thr	
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Val Gly Gly His Asn Cys Val Cys Lys Pro Gly Tyr Thr Gly Asn Gly	
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Thr Thr Cys Lys Ala Phe Cys Lys Asp Gly Cys Arg Asn Gly Gly Ala	
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Cys Arg Asp Gly Tyr His Asp Asn Gly Met Phe Ser Pro Ser Gly Glu	
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Ser Cys Glu Asp Ile Asp Glu Cys Gly Thr Gly Arg His Ser Cys Ala	
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Asn Asp Thr Ile Cys Phe Asn Leu Asp Gly Gly Tyr Asp Cys Arg Cys	

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Cys Ser Cys Gln Asn Gly Phe Val Met Cys Arg Arg Met Val Cys Asp							
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Cys Glu Asn Pro Thr Val Asp Leu Phe Cys Cys Pro Glu Cys Asp Pro							
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Arg Leu Ser Ser Gln Cys Leu His Gln Asn Gly Glu Thr Leu Tyr Asn							
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Ser Gly Asp Thr Trp Val Gln Asn Cys Gln Gln Cys Arg Cys Leu Gln							
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Gly Glu Val Asp Cys Trp Pro Leu Pro Cys Pro Asp Val Glu Cys Glu							
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Phe Ser Ile Leu Pro Glu Asn Glu Cys Cys Pro Arg Cys Val Thr Asp							
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Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp Ile Thr Lys Thr Cys Leu							
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 cgtgacatcc tgaaccctgg atagaaagcc tgagcccatt ggatctgtga aagcctctag 2864
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 actgcaagaa ataaaatgtc aggcagtga tgaattatat tttcagaagt aaagcaaaga 2984
 agctataaca tgttatgtac agtacactct gaaaagaaat ctgaaacaag ttattgtaat 3044
 gataaaaata atgcacaggc atggttactt aatattttct aacaggaaaa gtcaccccta 3104
 tttccttggt ttactgcact taatattatt tggttgaatt tgttcagtat aagctcgttc 3164
 ttgtgcaaaa ttaaataaat atttctctta cctt 3198

<210> 40
 <211> 499
 <212> PRT
 <213> Homo sapiens

<400> 40
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 Leu Glu Glu Ser Trp Glu His Ser Lys Glu Val Ser Glu Ala Glu Pro
 20 25 30
 Gly Gly Gly Ser Ser Gly Asp Ser Gly Pro Pro Glu Glu Ser Gly Gln
 35 40 45
 Glu Met Met Glu Glu Lys Glu Glu Ile Arg Lys Ser Lys Ser Val Ile
 50 55 60

Val 65	Pro	Ser	Gly	Ala	Pro 70	Lys	Lys	Glu	His	Val 75	Asn	Val	Val	Phe	Ile 80
Gly	His	Val	Asp	Ala 85	Gly	Lys	Ser	Thr	Ile 90	Gly	Gly	Gln	Ile	Met	Phe 95
Leu	Thr	Gly	Met 100	Ala	Asp	Lys	Arg	Thr 105	Leu	Glu	Lys	Tyr	Glu 110	Arg	Glu
Ala	Glu	Glu	Lys	Asn	Arg	Glu	Thr 120	Trp	Tyr	Leu	Ser	Trp 125	Ala	Leu	Asp
Thr	Asn 130	Gln	Glu	Glu	Arg	Asp 135	Lys	Gly	Lys	Thr	Val 140	Glu	Val	Gly	Arg
Ala 145	Tyr	Phe	Glu	Thr	Glu 150	Arg	Lys	His	Phe	Thr 155	Ile	Leu	Asp	Ala	Pro 160
Gly	His	Lys	Ser	Phe 165	Val	Pro	Asn	Met	Ile 170	Gly	Gly	Ala	Ser	Gln	Ala 175
Asp	Leu	Ala	Val 180	Leu	Val	Ile	Ser	Ala 185	Arg	Lys	Gly	Glu	Phe 190	Glu	Thr
Gly	Phe 195	Glu	Lys	Gly	Gly	Gln	Thr 200	Arg	Glu	His	Ala	Met 205	Phe	Gly	Lys
Thr 210	Ala	Gly	Val	Lys	His	Leu 215	Ile	Val	Leu	Ile	Asn 220	Lys	Met	Asp	Asp
Pro 225	Thr	Val	Asn	Trp	Gly 230	Ile	Glu	Arg	Tyr	Glu 235	Glu	Cys	Lys	Glu	Lys 240
Leu	Val	Pro	Phe	Leu 245	Lys	Lys	Val	Gly	Phe 250	Ser	Pro	Lys	Lys	Asp 255	Ile
His	Phe	Met	Pro 260	Cys	Ser	Gly	Leu	Thr 265	Gly	Ala	Asn	Ile	Lys 270	Glu	Gln
Ser	Asp	Phe 275	Cys	Pro	Trp	Tyr	Thr 280	Gly	Leu	Pro	Phe	Ile 285	Pro	Tyr	Leu
Asn 290	Asn	Leu	Pro	Asn	Phe	Asn 295	Arg	Ser	Ile	Asp	Gly 300	Pro	Ile	Arg	Leu
Pro	Ile	Val	Asp	Lys	Tyr	Lys	Asp	Met	Gly	Thr	Val	Val	Leu	Gly	Lys

305		310		315		320									
Leu	Glu	Ser	Gly	Ser	Ile	Phe	Lys	Gly	Gln	Gln	Leu	Val	Met	Met	Pro
				325					330					335	
Asn	Lys	His	Asn	Val	Glu	Val	Leu	Gly	Ile	Leu	Ser	Asp	Asp	Thr	Glu
			340					345					350		
Thr	Asp	Phe	Val	Ala	Pro	Gly	Glu	Asn	Leu	Lys	Ile	Arg	Leu	Lys	Gly
		355					360					365			
Ile	Glu	Glu	Glu	Glu	Ile	Leu	Pro	Glu	Phe	Ile	Leu	Cys	Asp	Pro	Ser
	370					375					380				
Asn	Leu	Cys	His	Ser	Gly	Arg	Thr	Phe	Asp	Val	Gln	Ile	Val	Ile	Ile
385					390					395					400
Glu	His	Lys	Ser	Ile	Ile	Cys	Pro	Gly	Tyr	Asn	Ala	Val	Leu	His	Ile
				405					410					415	
His	Thr	Cys	Ile	Glu	Glu	Val	Glu	Ile	Thr	Ala	Leu	Ile	Ser	Leu	Val
			420					425					430		
Asp	Lys	Lys	Ser	Gly	Glu	Lys	Ser	Lys	Thr	Arg	Pro	Arg	Phe	Val	Lys
		435					440					445			
Gln	Asp	Gln	Val	Cys	Ile	Ala	Arg	Leu	Arg	Thr	Ala	Gly	Thr	Ile	Cys
	450					455					460				
Leu	Glu	Thr	Phe	Lys	Asp	Phe	Pro	Gln	Met	Gly	Arg	Phe	Thr	Leu	Arg
465					470					475					480
Asp	Glu	Gly	Lys	Thr	Ile	Ala	Ile	Gly	Lys	Val	Leu	Lys	Leu	Val	Pro
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Glu	Lys	Asp													

<210> 41

<211> 1497

<212> DNA

<213> Homo sapiens

<400> 41

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 gggcccccag aagaaagtgg ccaggaaatg atggaggaaa aagaggaaat aagaaaatcc 180
 aaatctgtga tcgtaccctc aggtgcacct aagaaagaac acgtaaatgt agtattcatt 240
 ggccatgtag acgctggcaa gtcaaccatc ggaggacaga taatgttttt gactggaatg 300
 gctgacaaaa gaacactgga gaaatatgaa agagaagctg aggaaaaaaa cagagaaacc 360
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 gaagtgggtc gtgcctattt tgaaacagaa aggaacatt tcacaatttt agatgccctt 480
 ggccacaaga gttttgtccc aaatatgatt ggtggtgctt ctcaagctga tttggctgtg 540
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 agagaacatg cgatgtttgg caaacggca ggagtaaac atttaatagt gcttattaat 660
 aagatggatg atcccacagt aaattggggc atcgagagat atgaagaatg taaagaaaaa 720
 ctggtgccct ttttgaaaaa agtaggcttt agtccaaaaa aggacattca ctttatgccc 780
 tgctcaggac tgaccggagc aaatattaaa gagcagtcag atttctgccc ttggtacact 840
 ggattaccat ttattccgta tttgaataac ttgccaaact tcaacagatc aattgatgga 900
 ccaataagac tgccaattgt ggataagtac aaagatatgg gcactgtggt cctgggaaag 960
 ctggaatccg ggtccatttt taaaggccag cagctcgtga tgatgccaaa caagcacaat 1020
 gtagaagttc ttggaatact ttctgatgat actgaaactg attttgtagc cccaggtgaa 1080
 aacctcaaaa tcagactgaa ggaattgaa gaagaagaga ttcttccaga attcatactt 1140
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 gagcacaaat ccatcatctg cccaggttat aatgcggtgc tgcacattca tacttgtatt 1260
 gaggaagttg agataacagc gttaatctcc ttggtagaca aaaaatcagg ggaaaaaagt 1320
 aagacacgac cccgcttcgt gaaacaagat caagtatgca ttgctcgttt aaggacagca 1380
 ggaaccatct gcctcgagac gttcaaagat tttcctcaga tgggtcgttt tactttaaga 1440

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<210> 42

<211> 2057

<212> DNA

<213> Homo sapiens

<220>

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<222> (144)..(1640)

<400> 42

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aaggttccaa ttcagccggtt acc atg gaa ctt tca gaa cct gtt gta gaa aat 173

Met Glu Leu Ser Glu Pro Val Val Glu Asn

1

5

10

gga gag gtg gaa atg gcc cta gaa gaa tca tgg gag cac agt aaa gaa 221

Gly Glu Val Glu Met Ala Leu Glu Glu Ser Trp Glu His Ser Lys Glu

15

20

25

gta agt gaa gcc gag cct ggg ggt ggt tcc tcg gga gat tca ggg ccc 269

Val Ser Glu Ala Glu Pro Gly Gly Gly Ser Ser Gly Asp Ser Gly Pro

30

35

40

cca gaa gaa agt ggc cag gaa atg atg gag gaa aaa gag gaa ata aga 317

Pro Glu Glu Ser Gly Gln Glu Met Met Glu Glu Lys Glu Glu Ile Arg

45

50

55

aaa tcc aaa tct gtg atc gta ccc tca ggt gca cct aag aaa gaa cac 365

Lys Ser Lys Ser Val Ile Val Pro Ser Gly Ala Pro Lys Lys Glu His

60

65

70

gta aat gta gta ttc att ggc cat gta gac gct ggc aag tca acc atc 413

Val Asn Val Val Phe Ile Gly His Val Asp Ala Gly Lys Ser Thr Ile

75

80

85

90

gga gga cag ata atg ttt ttg act gga atg gct gac aaa aga aca ctg 461

Gly Gly Gln Ile Met Phe Leu Thr Gly Met Ala Asp Lys Arg Thr Leu

95						100						105						
gag	aaa	tat	gaa	aga	gaa	gct	gag	gaa	aaa	aac	aga	gaa	acc	tgg	tat	509		
Glu	Lys	Tyr	Glu	Arg	Glu	Ala	Glu	Glu	Lys	Asn	Arg	Glu	Thr	Trp	Tyr			
			110						115			120						
ttg	tcc	tgg	gcc	tta	gat	aca	aat	cag	gag	gaa	cga	gac	aag	ggg	aaa	557		
Leu	Ser	Trp	Ala	Leu	Asp	Thr	Asn	Gln	Glu	Glu	Arg	Asp	Lys	Gly	Lys			
			125						130			135						
aca	gtc	gaa	gtg	ggg	cgt	gcc	tat	ttt	gaa	aca	gaa	agg	aaa	cat	ttc	605		
Thr	Val	Glu	Val	Gly	Arg	Ala	Tyr	Phe	Glu	Thr	Glu	Arg	Lys	His	Phe			
			140						145			150						
aca	att	tta	gat	gcc	cct	ggc	cac	aag	agt	ttt	gtc	cca	aat	atg	att	653		
Thr	Ile	Leu	Asp	Ala	Pro	Gly	His	Lys	Ser	Phe	Val	Pro	Asn	Met	Ile			
			155						160			165			170			
ggg	ggg	gct	tct	caa	gct	gat	ttg	gct	gtg	ctg	gtc	atc	tct	gcc	agg	701		
Gly	Gly	Ala	Ser	Gln	Ala	Asp	Leu	Ala	Val	Leu	Val	Ile	Ser	Ala	Arg			
			175						180			185						
aaa	gga	gag	ttt	gaa	act	gga	ttt	gaa	aaa	ggg	gga	cag	aca	aga	gaa	749		
Lys	Gly	Glu	Phe	Glu	Thr	Gly	Phe	Glu	Lys	Gly	Gly	Gln	Thr	Arg	Glu			
			190						195			200						
cat	gcg	atg	ttt	ggc	aaa	acg	gca	gga	gta	aaa	cat	tta	ata	gtg	ctt	797		
His	Ala	Met	Phe	Gly	Lys	Thr	Ala	Gly	Val	Lys	His	Leu	Ile	Val	Leu			
			205						210			215						
att	aat	aag	atg	gat	gat	ccc	aca	gta	aat	tgg	ggc	atc	gag	aga	tat	845		
Ile	Asn	Lys	Met	Asp	Asp	Pro	Thr	Val	Asn	Trp	Gly	Ile	Glu	Arg	Tyr			
			220						225			230						
gaa	gaa	tgt	aaa	gaa	aaa	ctg	gtg	ccc	ttt	ttg	aaa	aaa	gta	ggc	ttt	893		
Glu	Glu	Cys	Lys	Glu	Lys	Leu	Val	Pro	Phe	Leu	Lys	Lys	Val	Gly	Phe			
			235						240			245			250			
agt	cca	aaa	aag	gac	att	cac	ttt	atg	ccc	tgc	tca	gga	ctg	acc	gga	941		
Ser	Pro	Lys	Lys	Asp	Ile	His	Phe	Met	Pro	Cys	Ser	Gly	Leu	Thr	Gly			
			255						260			265						
gca	aat	att	aaa	gag	cag	tca	gat	ttc	tgc	cct	tgg	tac	act	gga	tta	989		
Ala	Asn	Ile	Lys	Glu	Gln	Ser	Asp	Phe	Cys	Pro	Trp	Tyr	Thr	Gly	Leu			
			270						275			280						

cca	ttt	att	ccg	tat	ttg	aat	aac	ttg	cca	aac	ttc	aac	aga	tca	att	1037
Pro	Phe	Ile	Pro	Tyr	Leu	Asn	Asn	Leu	Pro	Asn	Phe	Asn	Arg	Ser	Ile	
		285					290					295				
gat	gga	cca	ata	aga	ctg	cca	att	gtg	gat	aag	tac	aaa	gat	atg	ggc	1085
Asp	Gly	Pro	Ile	Arg	Leu	Pro	Ile	Val	Asp	Lys	Tyr	Lys	Asp	Met	Gly	
	300					305					310					
act	gtg	gtc	ctg	gga	aag	ctg	gaa	tcc	ggg	tcc	att	ttt	aaa	ggc	cag	1133
Thr	Val	Val	Leu	Gly	Lys	Leu	Glu	Ser	Gly	Ser	Ile	Phe	Lys	Gly	Gln	
315					320					325					330	
cag	ctc	gtg	atg	atg	cca	aac	aag	cac	aat	gta	gaa	gtt	ctt	gga	ata	1181
Gln	Leu	Val	Met	Met	Pro	Asn	Lys	His	Asn	Val	Glu	Val	Leu	Gly	Ile	
				335					340					345		
ctt	tct	gat	gat	act	gaa	act	gat	ttt	gta	gcc	cca	ggg	gaa	aac	ctc	1229
Leu	Ser	Asp	Asp	Thr	Glu	Thr	Asp	Phe	Val	Ala	Pro	Gly	Glu	Asn	Leu	
			350					355					360			
aaa	atc	aga	ctg	aag	gga	att	gaa	gaa	gaa	gag	att	ctt	cca	gaa	ttc	1277
Lys	Ile	Arg	Leu	Lys	Gly	Ile	Glu	Glu	Glu	Glu	Ile	Leu	Pro	Glu	Phe	
		365					370					375				
ata	ctt	tgt	gat	cct	agt	aac	ctc	tgc	cat	tct	gga	cgc	acg	ttt	gat	1325
Ile	Leu	Cys	Asp	Pro	Ser	Asn	Leu	Cys	His	Ser	Gly	Arg	Thr	Phe	Asp	
	380					385					390					
gtt	cag	ata	gtg	att	att	gag	cac	aaa	tcc	atc	atc	tgc	cca	ggg	tat	1373
Val	Gln	Ile	Val	Ile	Ile	Glu	His	Lys	Ser	Ile	Ile	Cys	Pro	Gly	Tyr	
395					400					405					410	
aat	gcg	gtg	ctg	cac	att	cat	act	tgt	att	gag	gaa	gtt	gag	ata	aca	1421
Asn	Ala	Val	Leu	His	Ile	His	Thr	Cys	Ile	Glu	Glu	Val	Glu	Ile	Thr	
				415				420						425		
gcg	tta	atc	tcc	ttg	gta	gac	aaa	aaa	tca	ggg	gaa	aaa	agt	aag	aca	1469
Ala	Leu	Ile	Ser	Leu	Val	Asp	Lys	Lys	Ser	Gly	Glu	Lys	Ser	Lys	Thr	
			430					435					440			
cga	ccc	cgc	ttc	gtg	aaa	caa	gat	caa	gta	tgc	att	gct	cgt	tta	agg	1517
Arg	Pro	Arg	Phe	Val	Lys	Gln	Asp	Gln	Val	Cys	Ile	Ala	Arg	Leu	Arg	
		445					450					455				
aca	gca	gga	acc	atc	tgc	ctc	gag	acg	ttc	aaa	gat	ttt	cct	cag	atg	1565
Thr	Ala	Gly	Thr	Ile	Cys	Leu	Glu	Thr	Phe	Lys	Asp	Phe	Pro	Gln	Met	

460

465

470

ggt cgt ttt act tta aga gat gag ggt aag acc att gca att gga aaa 1613
 Gly Arg Phe Thr Leu Arg Asp Glu Gly Lys Thr Ile Ala Ile Gly Lys
 475 480 485 490

gtt ctg aaa ttg gtc cca gag aag gac taagcaattt tcttgatgcc 1660
 Val Leu Lys Leu Val Pro Glu Lys Asp
 495

tctgcaagat actgtgagga gaattgacag caaaagttca ccacctactc ttatttactg 1720
 cccattgatt gacttttctt catatttttgc aaagagaaat ttcacagcaa aaattcatgt 1780
 tttgtcagct ttctcatggt gagatctggt atgtcactga tgaatttacc ctcaagtttc 1840
 ctccctctgt accactctgc ttccttggac aatatcagta atagctttgt aagtgatgtg 1900
 gacgtaattg cctacagtaa taaaaaaata atgtacttta atttttcatt ttcttttagg 1960
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<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P1

<400> 43

acaccaatcc agtagccagg cttg

24

<210> 44

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P2

<400> 44

cactcgagaa tctgtgagac ctacatacat gacg

34

<210> 45

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (2)..(20)

<223> Xaa can be any naturally occurring amino acid

<400> 45

Cys	Xaa	Glu	Cys	Gly	Lys	Ala	Phe	Xaa	Gln	Lys	Ser	Xaa	Leu	Xaa	Xaa
1				5					10					15	

His	Gln	Arg	Xaa	His
			20	

<210> 46

<211> 7

<212> PRT

<213> Bovine sp.

<400> 46

Val	Leu	Asn	Ile	Ser	Leu	Trp
1				5		

<210> 47

<211> 17

<212> PRT

<213> Bovine sp.

<400> 47

Thr	Leu	Met	Glu	Leu	Leu	Asn	Gln	Met	Asp	Gly	Phe	Asp	Thr	Leu	His
1				5					10					15	

Arg

<210> 48

<211> 14
<212> PRT
<213> Bovine sp.

<220>
<221> misc_feature
<222> (11)..(13)
<223> Xaa can be any naturally occurring amino acid

<400> 48
Ala Val Ser Asp Phe Val Val Ser Glu Tyr Xaa Met Xaa Ala
1 5 10

<210> 49
<211> 9
<212> PRT
<213> Bovine sp.

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 49
Glu Val Asp Pro Leu Val Tyr Asn Xaa
1 5

<210> 50
<211> 11
<212> PRT
<213> Bovine sp.

<400> 50
His Gly Glu Ile Asp Tyr Glu Ala Ile Val Lys
1 5 10

<210> 51
<211> 25
<212> PRT
<213> Bovine sp.

<220>
<221> misc_feature

<222> (3)..(23)

<223> Xaa can be any naturally occurring amino acid

<400> 51

Leu	Ser	Xaa	Gly	Phe	Asn	Gly	Ala	Asp	Leu	Arg	Asn	Val	Xaa	Thr	Glu
1				5					10					15	

Ala	Gly	Met	Phe	Ala	Ile	Xaa	Ala	Asp
			20					25

<210> 52

<211> 21

<212> PRT

<213> Bovine sp.

<220>

<221> misc_feature

<222> (20)..(20)

<223> Xaa can be any naturally occurring amino acid

<400> 52

Met	Ile	Met	Ala	Thr	Asn	Arg	Pro	Asp	Thr	Leu	Asp	Pro	Ala	Leu	Leu
1				5					10					15	

Arg	Pro	Gly	Xaa	Leu
			20	

<210> 53

<211> 16

<212> PRT

<213> Bovine sp.

<400> 53

Ile	His	Ile	Asp	Leu	Pro	Asn	Glu	Gln	Ala	Arg	Leu	Asp	Ile	Leu	Lys
1				5					10					15	

<210> 54

<211> 11

<212> PRT

<213> Bovine sp.

<400> 54

Ala Thr Asn Gly Pro Arg Tyr Val Val Val Gly

1 5 10

<210> 55
<211> 7
<212> PRT
<213> Bovine sp.

<400> 55
Glu Ile Asp Gly Arg Leu Lys
1 5

<210> 56
<211> 14
<212> PRT
<213> Bovine sp.

<400> 56
Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val Leu Lys
1 5 10

<210> 57
<211> 8
<212> PRT
<213> Bovine sp.

<400> 57
Ile Leu Ala Gly Pro Ile Thr Lys
1 5

<210> 58
<211> 16
<212> PRT
<213> Bovine sp.

<220>
<221> misc_feature
<222> (1)..(2)
<223> Xaa can be any naturally occurring amino acid

<400> 58
Xaa Xaa Val Ile Glu Leu Pro Leu Thr Asn Pro Glu Leu Phe Gln Gly
1 5 10 15

<210> 59
<211> 9
<212> PRT
<213> Bovine sp.

<400> 59
Val Val Ser Ser Ser Leu Val Asp Lys
1 5

<210> 60
<211> 7
<212> PRT
<213> Bovine sp.

<400> 60
Ala Leu Gln Asp Tyr Arg Lys
1 5

<210> 61
<211> 7
<212> PRT
<213> Bovine sp.

<400> 61
Glu His Arg Glu Gln Leu Lys
1 5

<210> 62
<211> 12
<212> PRT
<213> Bovine sp.

<400> 62
Lys Leu Glu Ser Lys Leu Asp Tyr Lys Pro Val Arg
1 5 10

<210> 63
<211> 5
<212> PRT
<213> Bovine sp.

<400> 63

Leu Val Pro Thr Arg

1 5

<210> 64

<211> 11

<212> PRT

<213> Bovine sp.

<400> 64

Ala Lys Glu Glu Glu Ile Glu Ala Gln Ile Lys

1 5 10

<210> 65

<211> 10

<212> PRT

<213> Bovine sp.

<400> 65

Ala Asn Tyr Glu Val Leu Glu Ser Gln Lys

1 5 10

<210> 66

<211> 11

<212> PRT

<213> Bovine sp.

<400> 66

Val Glu Asp Ala Leu His Gln Leu His Ala Arg

1 5 10

<210> 67

<211> 8

<212> PRT

<213> Bovine sp.

<400> 67

Asp Val Asp Leu Tyr Gln Val Arg

1 5

<210> 68
<211> 13
<212> PRT
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<400> 68
Gln Ser Gln Gly Leu Ser Pro Ala Gln Ala Phe Ala Lys
1 5 10

<210> 69
<211> 21
<212> PRT
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<400> 69
Ala Gly Ser Gln Ser Gly Gly Ser Pro Glu Ala Ser Gly Val Thr Val
1 5 10 15

Ser Asp Val Gln Glu
20

<210> 70
<211> 12
<212> PRT
<213> Bovine sp.

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<400> 70
Gly Leu Leu Gly Xaa Asn Ile Ile Pro Leu Gln Arg
1 5 10

<210> 71
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer P1

<400> 71
ttgaagaatg atgcattagg aaccac 26

<210> 72
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer P2

<400> 72
cactcgagtg gctggatttc aatttctcca gtag 34

<210> 73
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer P3

<400> 73
gtcgagctag ccattctcctc ttcg 24

<210> 74
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer P4

<400> 74
catgggacgac aggttccgag acc 23

<210> 75
<211> 9
<212> PRT
<213> Homo sapiens

<400> 75

Lys Gly Ile Pro Ser Phe Trp Leu Thr
1 5

<210> 76

<211> 9

<212> PRT

<213> Saccharomyces sp.

<400> 76

Lys Gly Ile Pro Glu Phe Trp Leu Thr
1 5

<210> 77

<211> 10

<212> PRT

<213> Homo sapiens

<400> 77

Asp Ser Phe Phe Asn Phe Phe Ala Pro Pro
1 5 10

<210> 78

<211> 9

<212> PRT

<213> Saccharomyces sp.

<400> 78

Glu Ser Phe Phe Asn Phe Phe Ser Pro
1 5

<210> 79

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (2)..(11)

<223> Xaa can be any naturally occurring amino acid

<400> 79

Glu Xaa Xaa Lys Glu Xaa Pro Glu Val Lys Xaa Glu Glu Lys
1 5 10

<210> 80
<211> 5
<212> PRT
<213> HIV-1

<400> 80
Gly Arg Lys Lys Arg
1 5

<210> 81
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<213> Homo sapiens

<400> 81
Lys Lys Lys Arg Lys
1 5

<210> 82
<211> 25
<212> DNA
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<220>
<223> Description of Artificial Sequence: A1 Primer

<400> 82
cctaaaaagt gtctaagtgc cagtt 25

<210> 83
<211> 24
<212> DNA
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<220>
<223> Description of Artificial Sequence: A2 Primer

<400> 83
tcagtgaag ggaaggtaga acac 24

<210> 84
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence: P1 Primer

<400> 84
taatgaattt catttttagga ggtcgg 26

<210> 85
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<220>
<223> Description of Artificial Sequence: P2 Primer

<400> 85
atcttttggg aaagtaagat gagcc 25

<210> 86
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<220>
<223> Description of Artificial Sequence: C1 Primer

<400> 86
ggagactcac ctgctaattgt t 21

<210> 87
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: C4 Primer

<400> 87
ctcaaaagca gtctcttggc 20

<210> 88
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer A

<400> 88
atgggagata cagtagtgga gc 22

<210> 89
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer B

<400> 89
tcacatgatg ccgttggtga g 21

<210> 90
<211> 51
<212> DNA
<213> Homo sapiens

<400> 90
tggatcaagc caatacaaga ttcttgtgaa attacgactg atagtggcat g 51

<210> 91
<211> 117
<212> DNA
<213> Homo sapiens

<400> 91
tccatttggg aacaggagcg agtgcccctt tggatcaagc catacaagat tcttgtgatt 60

tcggctgata gtggcatgat tgaaccagtg gtcaatgctg tgtccatcca tcaggtg 117

<210> 92

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer C1

<400> 92

ctcagatcta tgggagatac agtagtggag c 31

<210> 93

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer C2

<400> 93

tcgagatctt cacatgatgc cgttggtgag 30

<210> 94

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: P1 Primer

<400> 94

gatttgctgct caataatcac tatctgaa 28

<210> 95

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: P2 Primer

<400> 95

ggttactagg atcacaaagt atgaattctg gaa

33

<210> 96

<211> 5

<212> PRT

<213> HIV-1

<400> 96

Tyr Arg Lys Lys Arg

1 5